

Amendments to the Claims:

The following "Listing of the Claims" will replace all prior versions and all prior listings of the claims in the present application:

Listing of The Claims:

Claims 1-31, previously cancelled.

32. Cancelled herein.

33. (Presently amended) A method for selecting a binding polypeptide from a repertoire of immunoglobulin superfamily polypeptides, said binding polypeptide comprising a first, target binding site and a second, generic ligand binding site, the method comprising the steps of:

- a) contacting the repertoire with the generic ligand to select polypeptides bound thereto, thereby obtaining a first selected pool of binding polypeptides; and
- b) contacting the first selected pool of binding polypeptides with a target ligand to select a population of polypeptides which bind to the target ligand.

34. (Previously added) The method of claim 33 wherein said repertoire of polypeptides is first contacted with said target ligand, and the resulting selected pool of binding polypeptides is then contacted with said generic ligand.

35. (Previously added) The method of claim 33 wherein said generic ligand binds a subset of the members of said repertoire of polypeptides.

36. Cancelled herein.

37. (Presently amended) The method of claim 36 33 wherein the binding polypeptide is an antibody or T-cell receptor polypeptide.

38. (Presently amended) The method of claim 36 33 wherein the binding polypeptide comprises V_H , V_β , V_L or V_α polypeptide sequence.

39. (Presently amended) The method of claim 36 33 wherein the binding polypeptide is an scFv polypeptide.
40. (Previously added) The method of claim 33 wherein said repertoire is comprised by phage particles.
41. (Previously added) The method of claim 40 wherein said phage particles comprise a fusion polypeptide.
42. (Previously added) The method of claim 33 wherein said generic ligand is a superantigen.
43. (Previously added) The method of claim 42 wherein said superantigen is selected from Protein A, Protein L and Protein G.
44. (Previously added) The method of claim 33 wherein polypeptides in said repertoire are varied at random positions.
45. (Previously added) The method of claim 44 wherein the variation is achieved by individually incorporating all 20 different amino acids at positions to be varied.
46. (Previously added) The method of claim 44 wherein the variation is achieved by individually incorporating fewer than all different amino acids at positions to be varied.
47. (Previously added) The method of claim 33 wherein polypeptides in said repertoire are varied at selected positions.
48. (Previously added) The method of claim 47 wherein said selected positions are comprised by the binding site for the target ligand.
49. (Previously added) The method of claim 47 wherein said selected positions are a subset of those within the binding site for the target ligand.
50. (Previously added) The method of claim 47 wherein the variation is achieved by individually incorporating all 20 different amino acids at positions to be varied.

51. (Previously added) The method of claim 47 wherein the variation is achieved by individually incorporating fewer than all different amino acids at positions to be varied.
52. (Previously amended) The method of claim 33 wherein step (a) further comprises the steps of:
 - i) contacting a second repertoire of polypeptides with a second, generic ligand to select polypeptides bound thereto, thereby obtaining a second selected pool of binding polypeptides, and
 - ii) combining said first and said second selected pools of binding polypeptides to create a third repertoire;
wherein step (b) comprises contacting said third repertoire with said target ligand to select a population of polypeptides which bind to said target ligand.